Evolved Digital Circuits and Genome Complexity

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The 2005 NASA/DoD Conference on Evolvable Hardware, June 29 - July 1, Washington DC, USA

Outline

- Introduction
 - Motivation
 - Artificial Development
 - Complexity
- **■** Experiments
 - Evolution of Circuits
 - Encoding Circuits
 - Measuring Complexity
- Results
 - Measured Complexity
- Conclusions
 - Conclusions and future work

Motivation

- Scalability issues in EHW
 - Limited to relatively small systems
 - Digital circuits, typically 3-4 bit multipliers and adders
 - Some ~100+ gates
 - Each new element in the genotype adds a dimension to the search space
- Limits the size and complexity achievable today through evolutionary approaches
- Possible improvements
 - · Hierarchical, Divide-and-conquer etc.
 - Tuning of representation and EA

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Artificial Development

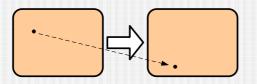
- Using direct mapping, one need large genotypes to describe large phenotypes
- The human genome consists of about 3 billion base pairs (109)
- The human brain is believed to contain about 10¹⁴-10¹⁵ synapses
- The process of biological development creates a complex creature from a (seemingly) less complex piece of information
- An indirect developmental mapping from genotype from phenotype
- This papers viewpoint with regards to scalability
 - Also self-organization, self-repair, gene regulatory networks etc.



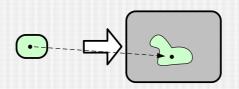








Direct mapping



Indirect mapping (deterministic)

Space of genotypes

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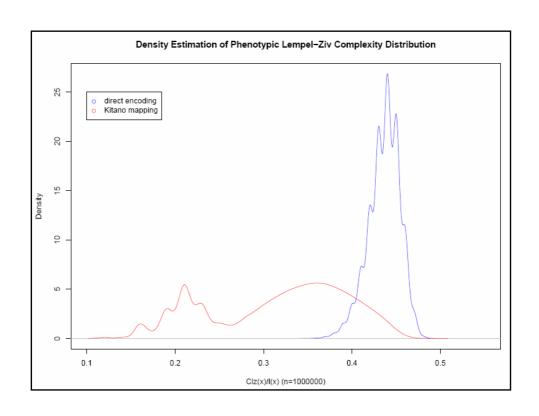
Complexity

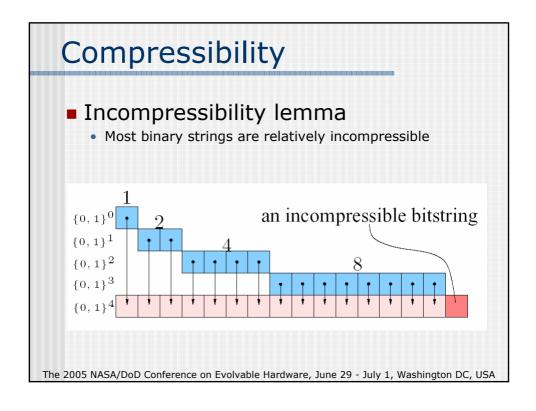
- Want large and complex designs
 - · Not just growth
- Measuring complexity (Lehre)
 - · Algorithmic complexity (Kolmogorov)
 - Length of the shortest program that can output the string
- This complexity is incomputable
 - Approximation; Lempel-Ziv compression
 - · Commonly used compression (zip)
 - LZ-complexity of a string is the length of its compressed version
- Measure the complexity of evolved circuits
 - Artificial development is a kind of decompression
 - Measuring complexity by compression indicates how small genotypes can be used to represent the relevant phenotypes
 - Are they suited for artificial development? (with regards to complexity)

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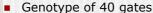
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Evolutionary Algorithm

- Cartesian Genetic Programming (J. Miller)
- Combinatorial circuits
 - 2-bit multiplier (200)
 - 2-bit adder (200)
- Evolutionary Algorithm
 - Tournament Selection (3/20)
 - Mutation rate 5%
 - Crossover rate 20%

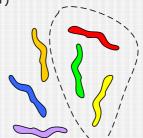


- NOR, NAND, OR, AND, NOT, VCC, GND
- Neutral elitism

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Encoding Circuits

- Need a binary representation to measure LZ-complexity
- Encode circuits
 - Straight-forward
 - One-Hot
 - Unused-to-Zero



Encoding Circuits

	SYMBOLIC				STRAIGHT			UNUSED-TO-ZERO				ONE-HOT		
label	type	in A	in B	type	in A	in B	type	active	in A	in B	type	in A	in B	
0														
1														
2														
3	4377	2				011				0.1	0001000		011	
4	AND	3	1	011	11	011	011	У	11	01	0001000	11	011	
5	NOT	4		010	100	000	000	n	000	000	0010000	100	00000	
6	OR	0	2	101	000	010	101	У	000	010	0000010	000	010	
7	NOR	2	1	110	010	001	110	У	010	001	0000001	010	001	
38	VCC			001	000000	000000	001	У	000000	000000	0100000	000000	000000	
39	GND			000	000000	000000	000	n	000000	000000	1000000	000000	000000	
40	NAND	30	22	100	011110	010110	000	n	000000	000000	0000100	011110	010110	
41	AND	15	27	011	001111	011011	011	y	001111	011011	0001000	001111	011011	
42	OR	37	34	101	100101	100010	101	v	100101	100010	0000010	100101	100010	
43	NAND	38	24	100	100110	011000	100	У	100110	011000	0000100	100110	011000	

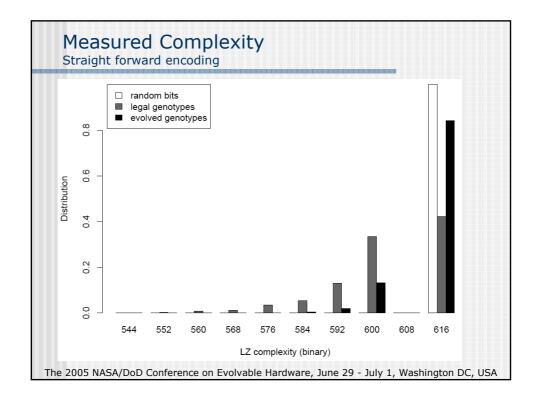
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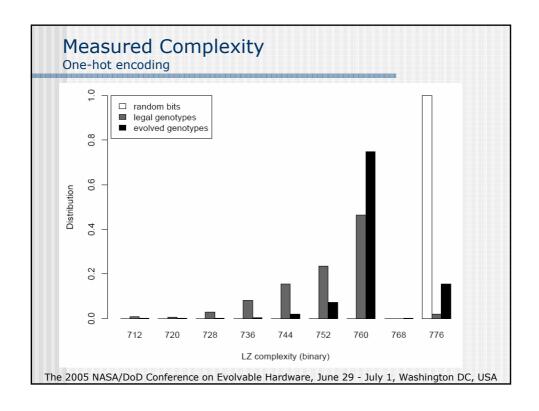
Measuring Complexity

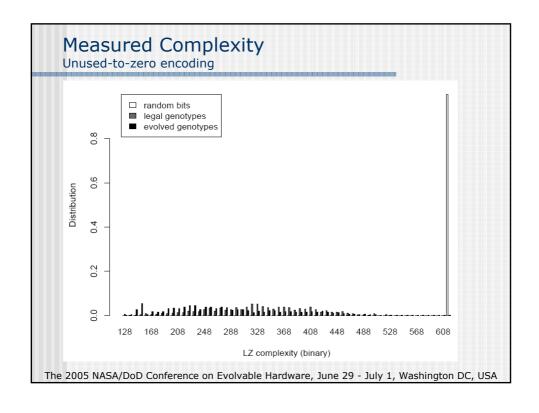
- LZ-complexity
 - Compress using zlib
 - Compresses to bytes
 - -> 8-bit granularity
- Measure the complexity of 200 evolved multipliers and adders
- Compare complexity of circuits to:
 - Random binary strings of the same length (10k)
 - Randomly selected legal genotypes (10k)
 - Search space complexity

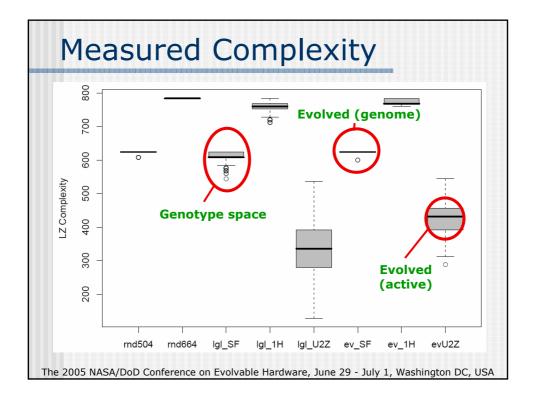
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Conclusions

- Implemented a measure for genotypic complexity of digital circuits
- Potential of reducing the search space by a huge factor... in theory
- LZ-decompression could act as an indirect mapping
- But...
 - · Large genotypes are not necessarily bad
 - Representation and mapping features
 - Search space structure
 - Distance-correlation

